



## INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

<b>(51) International Patent Classification <sup>7</sup> :</b> <b>C12Q 1/68</b>	<b>A1</b>	<b>(11) International Publication Number:</b> <b>WO 00/43540</b> <b>(43) International Publication Date:</b> 27 July 2000 (27.07.00)
<b>(21) International Application Number:</b> PCT/GB00/00146 <b>(22) International Filing Date:</b> 20 January 2000 (20.01.00) <b>(30) Priority Data:</b> 9901475.5      22 January 1999 (22.01.99)      GB <b>(71) Applicant (for all designated States except US):</b> PYROSEQUENCING AB [SE/SE]; Vallongatan 1, S-752 28 Uppsala (SE). <b>(71) Applicant (for GB only):</b> GARDNER, Rebeca [GB/GB]; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB). <b>(72) Inventor; and</b> <b>(75) Inventor/Applicant (for US only):</b> RONAGHI, Mostafa [SE/US]; Stanford DNA Sequencing & Technology Center, 855 California Avenue, Palo Alto, CA 94304 (US). <b>(74) Agents:</b> GARDNER, Rebecca et al.; Frank B. Dehn & Co., 179 Queen Victoria Street, London EC4V 4EL (GB).		<b>(81) Designated States:</b> AE, AL, AM, AT, AT (Utility model), AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, CZ (Utility model), DE, DE (Utility model), DK, DK (Utility model), DM, EE, EE (Utility model), ES, FI, FI (Utility model), GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KR (Utility model), KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK (Utility model), SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).  <b>Published</b> <i>With international search report.</i>
<b>(54) Title:</b> A METHOD OF DNA SEQUENCING		
<b>(57) Abstract</b>  <p>The present invention relates to a method of identifying a base at a target position in a sample nucleic acid sequence wherein a primer, which hybridises to the sample nucleic acid immediately adjacent to the target position, is provided and the sample nucleic acid and primer are subjected to a polymerase reaction in the presence of a nucleotide whereby the nucleotide will only become incorporated if it is complementary to the base in the target position, and said incorporation is detected, characterised in that, a single-stranded nucleic acid binding protein is included in the polymerase reaction step.</p> <div style="text-align: center; margin-top: 20px;"> <p>→ T C G G G G T G G G G C C C C G T C G C G G T C C →</p> </div> <div style="margin-top: 20px;"> <p><b>a</b></p> <p>A G T C A G T C A G T C A G T C A G T C A G T</p> <p><b>b</b></p> <p>A G T C A G T C A G T C A G T C A G T C A G T</p> <p><b>c</b></p> <p>A G T C A G T C A G T C A G T C A G T C A G T</p> </div>		